## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: Daggett, Lorrie P. Ellis, Steven B. - Liaw, Chen W. Lu, Chin-Chun
  - (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING SAME AND USES THEREFOR
  - (iii) NUMBER OF SEQUENCES: 21
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
    - (B) STREET: 444 South Flower Street, Suite 2000 (C) CITY: Los Angeles

    - (D) STATE: CA
    - (E) COUNTRY: U.S.A.
    - (F) ZIP: 90071-2921
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk

    - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE: 20-APR-1994
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/052,449
    - (B) FILING DATE: 20-APR-1993
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Reiter, Stephen E.
    - (B) REGISTRATION NUMBER: 31,192
    - (C) REFERENCE/DOCKET NUMBER: P41 9424
    - (ix) TELECOMMUNICATION INFORMATION:
      - (A) TELEPHONE: 619-546-4737
      - (B) TELEFAX: 619-546-9392
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4298 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: both
    - (D) TOPOLOGY: both
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 262..3078

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

• •				
CAAGCCGGGC GTTCC	GGAGCT GTGCCCGGC	C CCGCTTCAGC	ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGG	CCGAGC CCCCGCGCA	C GCTTCAGCCC	CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTC	CCGGGG GAGACGTGG	C GTCCGCAGCC	CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGG	CCCCGC GGGGGATGC	G CCGAGGGCCC	CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCC			CTG CTG ACG CTC GCC Leu Leu Thr Leu Ala 10	291
			TGC GAC CCC AAG ATC Cys Asp Pro Lys Ile 25	339
	Ala Val Leu Ser		CAC GAG CAG ATG TTC His Glu Gln Met Phe 40	387
		Lys Arg His	GGC TCC TGG AAG ATT Gly Ser Trp Lys Ile 55	435
_			AAC GCC ATC CAG ATG Asn Ala Ile Gln Met 70	483
			CAG GTC TAC GCC ATC Gln Val Tyr Ala Ile 90	531
			TTC ACT CCC ACC CCT Phe Thr Pro Thr Pro 105	579
			GTG CTG GGG CTG ACC Val Leu Gly Leu Thr 120	627
		Lys Ser Ile	CAC CTG AGC TTC CTG His Leu Ser Phe Leu 135	675
			GTG TGG TTT GAG ATG Val Trp Phe Glu Met 150	723
			CTG GTC AGC GAC GAC Leu Val Ser Asp Asp 170	771
			ACG CTG CTG GAG GAG Thr Leu Leu Glu Glu 185	819
CGT GAG TCC AAG Arg Glu Ser Lys 190	GCA GAG AAG GTG Ala Glu Lys Val	CTG CAG TTT Leu Gln Phe 195	GAC CCA GGG ACC AAG Asp Pro Gly Thr Lys 200	867
AAC GTG ACG GCC Asn Val Thr Ala 205	CTG CTG ATG GAG Leu Leu Met Glu 210	Ala Lys Glu	CTG GAG GCC CGG GTC Leu Glu Ala Arg Val 215	915

			AGC Ser							963
			ATG Met 240							1011
			GGG Gly							1059
			ATC Ile							1107
			GTG Val					_		1155
			CCG Pro							1203
			CTC Leu 320							1251
			GGT Gly							1299
	_		AGC Ser						_	1347
			AAT Asn							1395
			GGA Gly							1443
			ATT Ile 400							1491
			AGT Ser							1539
			AAG Lys							1587
			CGC Arg							1635
			ATC Ile							1683
			GCA Ala 480							1731

					AAG Lys											1779
					ATG Met											1827
			-		GAG Glu											1875
					AAG Lys											1923
					AGC Ser 560											1971
				_	ATG Met											2019
					AAC Asn								_			2067
			_		TGG Trp										_	2115
	_				CCC Pro											2163
					GCC Ala 640											2211
_			_		GTG Val								_		_	2259
					CTG Leu											2307
					TCC Ser											2355
					CGG Arg											2403
					GCC Ala 720											2451
					CTG Leu											2499
GTG Val	ACG Thr	ACT Thr	GGA Gly 750	GAG Glu	CTG Leu	TTT Phe	TTC Phe	CGC Arg 755	TCG Ser	GGC Gly	TTC Phe	GGC Gly	ATA Ile 760	GGC Gly	ATG Met	2547

CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Glm Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg 895 900 905	2979
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 910 915 920	3027
GAG AGG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 925 930 935	3075
TGAGACTCCC CGCCCGCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCCACG CAGAGCCCCC GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCGG GCAGCCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTCGCC CCTCCTCGGG	3795

CGCCTGCG	CT	CCTCTGCAGC	CTGAGCTCCA	CCCTCCCCTC	TTCTTGCGGC	ACCGCCCACC	3855
AAACACCC	CCG	TCTGCCCCTT	GACGCCACAC	GCCGGGGCTG	GCGCTGCCCT	CCCCACGGC	3915
CGTCCCTG	AC	TTCCCAGCTG	GCAGCGCCTC	CCGCCGCCTC	GGGCCGCCTC	CTCCAGAATC	3975
GAGAGGGC	TG	AGCCCCTCCT	CTCCTCGTCC	GGCCTGCAGC	ACAGAAGGGG	GCCTCCCCGG	4035
GGGTCCCC	CGG	ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	GGGCACGGGA	4095
GAGCGCCA	ACC	CGCCCGCCCC	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCCG	CCACCTTGTA	4155
CAGAACCA	AGC	ACTCCCAGGG	CCCGAGCGCG	TGCCTTCCCC	GTGCGCAGCC	GCGCTCTGCC	4215
CCTCCGTC	ccc	CAGGGTGCAG	GCGCGCACCG	CCCAACCCCC	ACCTCCCGGT	GTATGCAGTG	4275
GTGATGCC	CTA	AAGGAATGTC	ACG				4298

#### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUEN€E CHARACTERISTICS:
  - (A) LENGTH: 938 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 10 15 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala 165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu 180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met GlyThr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile 265 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Vak Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys 490 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met 505 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val 650 Leu Asp Arg Pro Glw Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala 705 710 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe 775 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val 805 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met 840 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser 885 890

Ser	Lys	Asp	Thr 900	Ser	Thr	Gly	Gly	Gly 905	Arg	Gly	Ala	Leu	Gln 910	Asn	Gln	
Lys	Asp	Thr 915	Val	Leu	Pro	Arg	Arg 920	Ala	Ile	Glu	Arg	Glu 925	Glu	Gly	Gln	
Leu	Gln 930	Leu	Суз	Ser -	Arg	His 935	Arg	Glu	Ser							
(2)				FOR CE CI												
		() ()	B) T: C) S:	engti YPE: IRANI OPOLO	nuc: DEDNI	leic ESS:	acid bot	đ								
	(ii)	MOI	LECUI	LE T	PE:	CDN	A									
	(ix)		A) N	E: AME/I OCAT			63								7	
	(xi	) SE	QUEN	CE DI	ESCR:	IPTI	: ис	SEQ	ID N	0:3:						
-				AAC Asn 5												48
		GGA Gly														63
(2)	INFO	ORMA!	гіои	FOR	SEQ	ID 1	NO:4	:								
	1	(i) :	(A (B	ENCE ) LEI ) TYI ) TOI	NGTH:	: 21 amino	amii	no ad id								
	( :	ii) 1	MOLE	CULE	TYP	E: p	cote:	in								
	()	кі) :	SEQUI	ENCE	DES	CRIP	CION	: SE	Q ID	NO:	4:					
Ser 1	Lys	Lys	Arg	Asn 5	Tyr	Glu	Asn	Leu	Asp 10	Gln	Leu	Ser	Tyr	Asp 15	Asn	
Lys	Arg	Gly	Pro 20	Lys												
(2)	INFO	ORMA	rion	FOR	SEQ	ID N	10:5	•								
	(i)	(I (I	A) LE B) TY C) ST	CE CH ENGTH PE: TRANI OPOLO	i: 43 nucl	840 k Leic ESS:	ase acio both	pai:	rs .							

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 189..3899

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	(xi)	SEC	QUENC	CE DI	ESCR	IPTIC	ON: S	SEQ :	ID NO	0:5:						~
CCCT	TAAT	CAA (	ATT?	rgcc	AC G	PACA	CTCG	A GC	CATC	GCGA	GTG	CCT:	rga (	GCCG	CGGGTG	60
ACGG	TGG	CTC ?	rcgc:	rgct	CG CC	GCCC	CCTC	C TC	CCGC	GGG	GGA	GCCT	GAT (	GCCA	CGTTCC	120
CTAT	GAA'	TA :	TTA:	rcgc	CG G	CCTA	AAAA:	r ac	CCCG	AACT	TCA	CAGC	CCG 2	AGTG	ACCCTC	180
CGGT	GGA	Met				a Le						u Le			G CTC r Leu	230
TTC ( Phe (																278
ACG (																326
CGT (																374
CAG Gln																422
ACC (																470
TTT (Phe 95																518
ATC 1																566
GCT (																614
GGC (																662
GAG '																710
CAC (His 175																758
GTG 7																806

( ,

													GAC Asp 220	_		854
													CTC Leu			902
													TGG Trp			950
													ACC Thr			998
													AGC Ser			1046
													GCC Ala 300			1094
													GAC Asp			1142
													TAC Tyr			1190
													AGC Ser			1238
													AAC Asn			1286
													CTA Leu 380			1334
													CCT Pro			1382
													ccc Pro			1430
													CCC Pro			1478
													GGG Gly			1526
													GAC Asp 460			1574
AAG Lys	AAG Lys	CTG Leu 465	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys 470	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu 475	TAC Tyr	CTG Leu	GTG Val	1622

ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
					Gly											
					TAC Tyr 500											1718
					CGC Arg											1766
					AGT Ser											1814
					TTG Leu											1862
					CTC Leu											1910
					GTC Val 580											1958
					GCT Ala											2006
					AAC Asn											2054
					ATG Met											2102
					ACG Thr											2150
_					GTG Val 660											2198
					CCA Pro											2246
					ATC Ile											2294
					CAG Gln											2342
AAG Lys	ATG Met 720	GGG Gly	AAG Lys	CTG Leu	GAT Asp	GCC Ala 725	TTC Phe	ATC Ile	TAT Tyr	GAT Asp	GCT Ala 730	GCT Ala	GTC Val	CTC Leu	AAC Asn	2390
					GAC Asp 740											2438

				TAC Tyr						2486
				CTG Leu 775						2534
				ACA Thr						2582
 	 			AGC Ser						2630
				CTG Leu						2678
				GTC Val						2726
				TTC Phe 855						2774
				CAG Gln						2822
				AGC Ser						2870
				ATG Met						2918
-				ACC Thr						2966
				TGC Cys 935						3014
				CCG Pro						3062
				CGC Arg						3110
				ACG Thr						3158
				GCC Ala		Glu			Val	3206
		Cys		CTC Leu 1015	Ser			Pro		3254

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025	3302
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG Cys Thr Gly Pro Ara Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser 1170 1180	3734
GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG	3986
CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT	4046
CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTTGCTGTC CTCTTCTCAC	4106
GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT	4166
GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA	4226

GGCAGGGCCA	TCCCGATCCT	TGCTCTACCT	GGCTAGAGTT	TCTTCTCATC	AGAGCACTGG	4286
GACATTAAAC	CCACCTTTTC	CCAGAAAAA	АААААААА	АААААААА	AAAG	4340

### (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1236 amino acids

  - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val Ser Leu Glu Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala 165 170 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser 185

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro 200

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly 265

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys 280 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu 330 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser 390 395 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile 505 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe 555 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala 600 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr

. . .

Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys 745 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val 825 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr 855 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro 935 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln

- Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser 980 985 990
- Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr 995 1000 1005
- Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro 1010 1015 1020
- Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg 1025 1030 1035 1040
- Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro 1045 1050 1055
- Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala 1060 1065 1070
- Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser 1075 1080 1085
- Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr 1090 1095 1100
- Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu 1105 1110 1115 1120
- Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln 1125 1130 1135
- Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val 1140 1145 1150
- Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys 1155 1160 1165
- Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala 1170 1175 1180
- Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly 1185
- Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly 1205 1210 1215
- Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu 1220 1225 1230

Glu Ser Glu Val 1235

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: both
    - (D) TOPOLOGY: both
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
C TCT GAG GCT CAG CCT GTC CCC AG Ser Glu Ala Gln Pro Val Pro 1 5	24
(2) INFORMATION FOR SEQ ID NO:8:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 7 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
Ser Glu Ala Gln Pro Val Pro 1 5	
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 11 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: unknown  (D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(ALL) CROUDINGS DECONTRACTOR, CRO. ID NO. 9.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
AGAAGGGGT G	11
	11
AGAAGGGGT G	11
AGAAGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 4808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both	11
AGAAGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 4808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	11
AGAAGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 4808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (ix) FEATURE:  (A) NAME/KEY: CDS	11
AGAAGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 4808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (ix) FEATURE:  (A) NAME/KEY: CDS  (B) LOCATION: 3114705	11
AGAAGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 4808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (ix) FEATURE:  (A) NAME/KEY: CDS  (B) LOCATION: 3114705  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
AGAAGGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:	60
AGAAGGGGGT G  (2) INFORMATION FOR SEQ ID NO:10:  (i) SEQUENCE CHARACTERISTICS:	60 120

AG	rggc	GACT	ATG	GGC Gly	AGA	GTG	GGC	TAT	TGG	ACC	CTG	CTG	GTG	CTG	CCG	349
			1				5					10				
GCC Ala	CTT Let 15	ı Let	G GTO	TGG Trp	CGC Arg	GGT Gly 20	Pro	GCC Ala	CCC Pro	AGO Ser	G GCG Ala 25	a Ala	G GCO A Ala	G GAG	G AAG 1 Lys	397
GGT Gly 30	Pro	C CCC	C GCG Ala	CTA Leu	AAT Asr 35	ılle	GCG Ala	GTO Val	ATO Met	CTC Let	Gly	CAC His	C AGG	C CAC	C GAC s Asp 45	445
GTC Val	ACI Thi	A GAC	G CGC	GAA Glu 50	Leu	CGA Arg	ACA Thr	CTC Leu	TGG Trp 55	Gly	C CCC	GA(	G CAC	G GCG n Ala 60	G GCG a Ala	493
GGG	CTC Leu	CCC Pro	CTG Leu 65	Asp	GTG Val	AAC Asn	GTG Val	GTA Val 70	Ala	CTC Leu	CTO Lev	ATO Met	AAC Asr 75	Arç	C ACC	541
GAC	CCC Pro	AAG Lys 80	Ser	CTC Leu	ATC Ile	ACG Thr	CAC His 85	Val	TGC	GAC	CTC Leu	ATC Met	Ser	GGG Gly	GCA Ala	589
CGC Arg	ATC Ile 95	His	GGC Gly	CTC Leu	GTG Val	TTT Phe 100	Gly	GAC Asp	GAC Asp	ACG Thr	GAC Asp 105	Glr	GAG Glu	GCC	GTA Val	637
GCC Ala 110	GIn	ATG Met	CTG Leu	GAT Asp	TTT Phe 115	Ile	TCC Ser	TCC Ser	CAC His	ACC Thr 120	Phe	GTC Val	CCC Pro	ATC Ile	TTG Leu 125	685
GGC Gly	ATT Ile	CAT His	GGG Gly	GGC Gly 130	GCA Ala	TCT Ser	ATG Met	ATC Ile	ATG Met 135	GCT Ala	GAC Asp	AAG Lys	GAT Asp	CCG Pro	ACG Thr	733
TCT Ser	ACC Thr	TTC Phe	TTC Phe 145	CAG Gln	TTT Phe	GGA Gly	GCG Ala	TCC Ser 150	ATC Ile	CAG Gln	CAG Gln	CAA Gln	GCC Ala 155	ACG Thr	GTC Val	781
ATG Met	CTG Leu	AAG Lys 160	ATC	ATG Met	CAG Gln	GAT Asp	TAT Tyr 165	GAC Asp	TGG Trp	CAT His	GTC Val	TTC Phe 170	TCC Ser	CTG Leu	GTG Val	829
ACC Thr	ACT Thr 175	ATC Ile	TTC Phe	CCT Pro	GGC Gly	TAC Tyr 180	AGG Arg	GAA Glu	TTC Phe	ATC Ile	AGC Ser 185	TTC Phe	GTC Val	AAG Lys	ACC Thr	877
ACA Thr 190	GTG Val	GAC Asp	AAC Asn	AGC Ser	TTT Phe 195	GTG Val	GGC Gly	TGG Trp	GAC Asp	ATG Met 200	CAG Gln	AAT Asn	GTG Val	ATC Ile	ACA Thr 205	925
CTG Leu	GAC Asp	ACT Thr	TCC Ser	TTT Phe 210	GAG Glu	GAT Asp	GCA Ala	AAG Lys	ACA Thr 215	CAA Gln	GTC Val	CAG Gln	CTG Leu	AAG Lys 220	AAG Lys	973
ATC Ile	CAC His	TCT Ser	TCT Ser 225	GTC Val	ATC Ile	TTG Leu	CTC Leu	TAC Tyr 230	TGT Cys	TCC Ser	AAA Lys	GAC Asp	GAG Glu 235	GCT Ala	GTT Val	1021
CTC Leu	ATT Ile	CTG Leu 240	AGT Ser	GAG Glu	GCC Ala	CGC Arg	TCC Ser 245	CTT Leu	GGC Gly	CTC Leu	ACC Thr	GGG Gly 250	TAT Tyr	GAT Asp	TTC Phe	1069
File	TGG Trp 255	ATT Ile	GTC Val	CCC Pro	Ser	TTG Leu 260	GTC Val	TCT Ser	GGG Gly	Asn	ACG Thr	GAG Glu	CTC Leu	ATC Ile	CCA Pro	1117

		GGA Gly 275						1165
		AGA Arg						1213
		CTG Leu						1261
		CAG Gln						1309
		GTC Val						1357
		TAC Tyr 355						1405
		GAA Glu						1453
		CAC His						1501
		GAC Asp						1549
		GTG Val						1597
		CCA Pro 435						1645
		AAT Asn					 	1693
		CTT Leu						1741
		GGG Gly						1789
		GAA Glu						1837
		AAT Asn 515						1885
		ACG Thr						1933

GGC	ACC	CTC	<b>ም</b> ሮኔ	CCT	ጥርጥ	GCT	ሙጥጥ	ΔΨΩ	CAA	CCA	ጥጥር	AGC	GCC	ጥርጥ	GTC	1981
						Ala										1701
						ATG Met										2029
						AGC Ser 580										2077
						GGG Gly										2125
						GTG Val										2173
						AAG Lys										2221
						AGC Ser										2269
						GAC Asp 660										2317
						TAT Tyr										2365
						AGA Arg										2413
						TTT Phe										2461
		-				AAG Lys	-			_					-	2509
						GGG Gly 740										2557
						TTT Phe										2605
						AAG Lys										2653
						ATG Met										2701
						AAG Lys										2749

	GAC Asp 815															2797
	AGC Ser				-											2845
	TTC Phe															2893
	ATC Ile													_	_	2941
	AAG Lys															2989
	TTA Leu 895															3037
	AAC Asn															3085
	AGA Arg															3133
	TAC Tyr															3181
	AAC Asn															3229
	CTC Leu 975															3277
	TCC Ser										Ser					3325
	AAC Asn				Arg					Lys					Ile	3373
	CAG Gln			Leu					Val					Glu		3421
	GCA Ala		Asn					Leu					Tyr			3469
	GAG Glu 1055	Met					Ile					Asn				3517
TGC Cys 1070	CAC His	AGG Arg	GAA Glu	CCT Pro	GAC Asp 1075	Asn	AGT Ser	AAG Lys	AAC Asn	CAC His 1080	Lys	ACC Thr	AAG Lys	GAC Asp	AAC Asn 1085	3565

TTT AAA AGG Phe Lys Arg	TCA GTG GCC Ser Val Ala 1090	TCC AAA TA Ser Lys Ty	C CCC AAG GAC r Pro Lys Asp 1095	C TGT AGT GAG Cys Ser Glu 110	ı Val
GAG CGC ACC Glu Arg Thr	TAC CTG AAA Tyr Leu Lys 1105	ACC AAA TC Thr Lys Se 11	A AGC TCC CCT r Ser Ser Pro 10	AGA GAC AAG Arg Asp Lys 1115	G ATC 3661 3 Ile
TAC ACT ATA Tyr Thr Ile 1120	Asp Gly Glu	AAG GAG CC Lys Glu Pr 1125	T GGT TTC CAC o Gly Phe His	TTA GAT CCA Leu Asp Pro 1130	A CCC 3709 Pro
CAG TTT GTT Gln Phe Val 1135	GAA AAT GTG Glu Asn Val	ACC CTG CC Thr Leu Pr 1140	C GAG AAC GTG o Glu Asn Val 114	. Asp Phe Pro	G GAC 3757 O Asp
CCC TAC CAG Pro Tyr Gln 1150	GAT CCC AGT Asp Pro Ser 115	Glu Asn Ph	C CGC AAG GGG e Arg Lys Gly 1160	GAC TCC ACC Asp Ser Thr	CTG 3805 Leu 1165
CCA ATG AAC Pro Met Asn	CGG AAC CCC Arg Asn Pro ~1170	TTG CAT AA' Leu His Ası	T GAA GAG GGG n Glu Glu Gly 1175	CTT TCC AAC Leu Ser Asn 118	Asn
Asp Gin Tyr	AAA CTC TAC Lys Leu Tyr 1185	TCC AAG CAG Ser Lys His	C TTC ACC TTG S Phe Thr Leu 90	AAA GAC AAG Lys Asp Lys 1195	GGT 3901 Gly
TCC CCG CAC : Ser Pro His : 1200	Ser Glu Thr	AGC GAG CGA Ser Glu Arc 1205	A TAC CGG CAG J Tyr Arg Gln	AAC TCC ACG Asn Ser Thr 1210	CAC 3949 His
TGC AGA AGC ( Cys Arg Ser ( 1215	Cys Leu Ser	Asn Met Pro 1220	Thr Tyr Ser 122	Gly His Phe 5	Thr
ATG AGG TCC ( Met Arg Ser I 1230	Pro Phe Lys 1235	Cys Asp Ala	Cys Leu Arg 1240	Met Gly Asn	Leu 1245
TAT GAC ATC O	Asp Glu Asp 1250	Gln Met Leu	Gln Glu Thr 1255	Gly Asn Pro 126	Ala O
	31n Val Tyr 1265	Gln Gln Asp 127	Trp Ala Gln	Asn Asn Ala 1275	Leu
CAA TTA CAA A Gln Leu Gln I 1280	Lys Asn Lys	Leu Arg Ile 1285	Ser Arg Gln	His Ser Tyr 1290	Asp
AAC ATT GTC G Asn Ile Val A 1295	sp Lys Pro	Arg Glu Leu 1300	Asp Leu Ser 1305	Arg Pro Ser	Arg
AGC ATA AGC C Ser Ile Ser L 1310	eu Lys Asp 1 1315	Arg Glu Arg	Leu Leu Glu 1320	Gly Asn Phe	Tyr 1325
GGC AGC CTG TG Gly Ser Leu P	1330	ro Ser Ser	Lys Leu Ser	Gly Lys Lys 1340	Ser
TCC CTT TTC Co	CC CAA GGT ( ro Gln Gly I 345	CTG GAG GAC Leu Glu Asp 1350	Ser Lys Arg	AGC AAG TCT Ser Lys Ser 1355	CTC 4381 Leu

			His					Pro					His	AGG Arg		4429
		Arg					Arg					Pro		AAA Lys		4477
	Leu					Val					Leu			TCC Ser		4525
				-	Tyr					Ser				AAT Asn 1420	Asp	4573
				Glu					Tyr					AAT Asn 5		4621
			Thr					Asn					Arg	CGC Arg		4669
		Glu		CCT Pro			Glu				TAA <i>I</i> 146	TAAL	CTT (	CCAT'	<b>FAATGT</b>	4722
TTT	ATCT?	ATA (	GGA	AATA	CA CO	TAAT	rggc	C AA	rgtt	CTGG	AGG	TAA	ATG :	rtgg/	ATGTCC	4782
AAT	GTG	ecc s	rgctz	AAGA	GG A	AGGA	3									4808

# (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1464 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu 1 5 10 15

Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro 20 25 30

Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$ 

Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro 50 55 60

Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys
65 70 75 80

Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His 85 90 95

Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met
100 105 110

Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His
115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe 135 Phe Gln Phe Gly Ala Ser Ile Gln Gln Ala Thr Val Met Leu Lys 155 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp 185 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu 230 235 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp 11e Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu 340 345 350 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn 425 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 455 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val 535 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys 585 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu 600 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly 615 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu 650 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser 740 745 750 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu 820

825

830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys 835 840 845

Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser 850 855 860

Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys 865 870 875

Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys 885 890 895

Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser 900 905 910

Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly 915 920 925

Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser 930 935 940

Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met 945 950 955 960

Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn 965 970 975

Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn 980 985 990

Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser 995 1000 1005

Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp 1010 1015 1020

Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu 1025 1030 1035 1040

Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met 1045 1050 1055

Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg 1060 1065 1070

Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg 1075 1080 1085

Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr 1090 1095 1100

Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile 1105 1110 1115 1120

Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val 1125 1130 1135

Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln 1140 1145 1150

Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn 1155 1160 1165

Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr 1170 1175 1180 Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His 1185 1190 1195 1200

Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser 1205 1210 1215

Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser 1220 1225 1230

Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile 1235 1240 1245

Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu 1250 1260

Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln 1265 1270 1275 1280

Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val 1285 1290 1295

Asp Lys Pro Arg Glu-Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser 1300 1305 1310

Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu 1315 1320 1325

Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe 1330 1335 1340

Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp 1345 1350 1355 1360

His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
1365 1370 1375

Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro 1380 1385 1390

Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr 1395 1400 1405

Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile 1410 1415 1420

Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser 1425 1430 1435 1440

Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu 1445 1450 1455

Met Pro Ser Ile Glu Ser Asp Val 1460

#### (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
CGAGGGAGGC GGCCGCGCG GACTCTCTC GCGGGCGCAG CGCCCCTTCC CCCTCGGA	ACC 60
CTCCGGTGGA CATG	74
(2) INFORMATION FOR SEQ ID NO:13:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 5538 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: both	
(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA	
(ix) FEATURE:	
(A) NAME/KEY: CDS (B) LOCATION: 2104664	
· · · · · · · · · · · · · · · · · · ·	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATT	TTT 60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAC	GAA 120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCT	TTC 180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT	
Met Lys Pro Arg Ala Glu Cys Cys 1 5	3
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC	
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser 10 15 20	;
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC	329
Arg Ala Arg Ser.Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile 25 30 35 40	
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAF	A 377
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys 45 50 55	;
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC	2 425
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala 60 65 70	
ATG AAT GAG ACC GAC CCA AAG AGC ATC ACC CGC ATC TGT GAT CTC Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu	
75 80 85	
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp	
90 95 100	
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu	
105 110 115 120	

ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp 125

		ATG Met						665
		CTC Leu						713
		ACC Thr						761
		ATT Ile 190						809
		GAC Asp						857
		AAA Lys						905
		ACC Thr						953
		TAC Tyr						1001
		CCT Pro 270						1049
		GAC Asp						1097
		ACT Thr						1145
		AAA Lys						1193
		ATG Met						1241
		TCC Ser 350						1289
		CTT Leu						1337
		AAG Lys						1385
		ACT Thr						1433

ACC Thr 410									1481
AGT Ser									1529
ACT Thr									1577
AAG Lys									1625
TTC Phe									1673
ATC Ile 490									1721
GCC Ala									1769
GTG Val									1817
GTG Val									1865
TTC Phe									1913
TCA Ser 570									1961
AAC Asn								:	2009
ATC Ile								:	2057
GTA Val								:	2105
GTG Val								:	2153
TTA Leu 650								:	2201
CTG Leu								:	2249

							AAT Asn		2297
							AAC Asn 710		2345
							CTG Leu		2393
							AGA Arg		2441
							GCT Ala		2489
							CGC Arg		2537
							GAA Glu 790		2585
							AAT Asn		2633
							TTC Phe		2681
							TGC Cys		2729
							TGT Cys		2777
	_				_		AGC Ser 870	_	2825
							TCC Ser		2873
							CTG Leu		2921
							CCG Pro		2969
							ATC Ile		3017
							AAC Asn 950		3065

CCC Pro	TGT Cys	GAG Glu 955	GAG Glu	AAC Asn	CTC Leu	TTC Phe	AGT Ser 960	GAC Asp	TAC Tyr	ATC Ile	AGT Ser	GAG Glu 965	GTA Val	GAG Glu	AGA Arg	3113
ACG Thr	TTC Phe 970	GGG Gly	AAC Asn	CTG Leu	CAG Gln	CTG Leu 975	AAG Lys	GAC Asp	AGC Ser	AAC Asn	GTG Val 980	TAC Tyr	CAA Gln	GAT Asp	CAC His	3161
TAC Tyr 985	CAC His	CAT His	CAC His	CAC His	CGG Arg 990	ccc Pro	CAT His	AGT Ser	ATT Ile	GGC Gly 995	AGT Ser	GCC Ala	AGC Ser	TCC Ser	ATC Ile 1000	3209
GAT Asp	GGG Gly	CTC Leu	TAC Tyr	GAC Asp 1005	Cys	GAC Asp	AAC Asn	CCA Pro	CCC Pro 1010	Phe	ACC Thr	ACC Thr	CAG Gln	TCC Ser 1015	Arg	3257
TCC Ser	ATC Ile	AGC Ser	AAG Lys 1020	Lys	CCC Pro	CTG Leu	GAC Asp	ATC Ile 1025	Gly	CTC Leu	CCC Pro	TCC Ser	TCC Ser 1030	Lys	CAC His	3305
AGC Ser	CAG Gln	CTC Leu 103	Ser	GAC Asp	CTG Leu	TAC Tyr	GGC Gly 1040	Lys	TTC Phe	TCC Ser	TTC Phe	AAG Lys 104	Ser	GAC Asp	CGC Arg	3353
TAC Tyr	AGT Ser 105	Gly	CAC His	GAC Asp	GAC Asp	TTG Leu 105	Ile	CGC Arg	TCC Ser	GAT Asp	GTC Val 106	Ser	GAC Asp	ATC Ile	TCA Ser	3401
ACC Thr 106	CAC His 5	ACC Thr	GTC Val	ACC Thr	TAT Tyr 107	Gly	AAC Asn	ATC Ile	GAG Glu	GGC Gly 107	Asn	GCC Ala	GCC Ala	AAG Lys	AGG Arg 1080	3449
CGT Arg	AAG Lys	CAG Gln	CAA Gln	TAT Tyr 108	Lys	GAC Asp	AGC Ser	CTG Leu	AAG Lys 109	Lys	CGG Arg	CCT Pro	GCC Ala	TCG Ser 109	Ala	3497
AAG Lys	TCC Ser	CGC Arg	AGG Arg 110	Glu	TTT Phe	GAC Asp	GAG Glu	ATC Ile 110	Glu	CTG Leu	GCC Ala	TAC Tyr	CGT Arg 111	Arg	CGA Arg	3545
CCC	CCC Pro	CGC Arg 111	Ser	CCT Pro	GAC Asp	CAC His	AAG Lys 112	Arg	TAC Tyr	TTC Phe	AGG Arg	GAC Asp 112	Lys	GAA Glu	GGG Gly	3593
Lev	CGG Arg 113	Asp	Phe	Tyr	Leu	Asp	Gln	Phe	Arg	Thr	Lys	Glu	AAC Asn	TCA Ser	CCC Pro	3641
CAC His 114	Trp	GAG Glu	CAC His	GTA Val	GAC Asp 115	Leu	ACC Thr	GAC	ATC Ile	TAC Tyr 115	Lys	GAG Glu	CGG Arg	AGT Ser	GAT Asp 1160	3689
GA( As)	TTT Phe	AAG Lys	CGC Arg	GAC Asp 116	Ser	ATC	AGC Ser	GGA Gly	GGA Gly 117	Gly	ccc Pro	TGT Cys	ACC	AAC Asn 117	AGG Arg 5	3737
TC? Se:	CAC His	ATC	AAG Lys	His	GGG Gly	ACG Thr	GGC Gly	GAC Asp 118	Lys	CAC His	GGC Gly	GTG Val	GTC Val 119	Ser	GGG Gly	3785
GTI Va	A CCT	GCA Ala 119	Pro	TGG Trp	GAG Glu	AAG Lys	AAC Asn 120	Leu	ACC Thr	AAC Asn	GTG Val	GAG Glu 120	Trp	GAG Glu	GAC Asp	3833
CGG	G TCC g Ser 121	Gly	GGC Gly	AAC Asn	TTC Phe	TGC Cys 121	Arg	AGC Ser	TGT Cys	CCC Pro	TCC Ser 122	Lys	CTG Leu	CAC His	AAC Asn	3881

TAC TCC ACG ACG GTG ACG Tyr Ser Thr Thr Val Thr 1225 123	: Gly Gln Asn Ser	Gly Arg Gln Ala Cys	ATC 3929 Ile 1240
CGG TGT GAG GCT TGC AAC Arg Cys Glu Ala Cys Lys 1245	AAA GCA GGC AAC Lys Ala Gly Asn 125	Leu Tyr Asp Ile Ser	GAG 3977 Glu
GAC AAC TCC CTG CAG GAA Asp Asn Ser Leu Gln Glu 1260	A CTG GAC CAG CCG Leu Asp Gln Pro 1265	GCT GCC CCA GTG GCG Ala Ala Pro Val Ala 1270	GTG 4025 Val
ACG TCA AAC GCC TCC ACC Thr Ser Asn Ala Ser Thr 1275	C ACT AAG TAC CCT Thr Lys Tyr Pro 1280	CAG AGC CCG ACT AAT Gln Ser Pro Thr Asn 1285	TCC 4073 Ser
AAG GCC CAG AAG AAG AAG Lys Ala Gln Lys Lys Ass 1290	C CGG AAC AAA CTG n Arg Asn Lys Leu 1295	CGC CGG CAG CAC TCC Arg Arg Gln His Ser 1300	TAC 4121 Tyr
GAC ACC TTC GTG GAC CTC Asp Thr Phe Val Asp Let 1305	ı Gln Lys Glu Glu	GCC GCC CTG GCC CCG Ala Ala Leu Ala Pro 1315	CGC 4169 Arg 1320
AGC GTA AGC CTG AAA GA Ser Val Ser Leu Lys As 1325	C AAG GGC CGA TTC p Lys Gly Arg Phe 133	Met Asp Gly Ser Pro	Tyr
GCC CAC ATG TTT GAG ATG Ala His Met Phe Glu Me 1340	G TCA GCT GGC GAG t Ser Ala Gly Glu 1345	AGC ACC TTT GCC AAC Ser Thr Phe Ala Asn 1350	AAC 4265 Asn
AAG TCC TCA GTG CCC AC Lys Ser Ser Val Pro Th 1355	T GCC GGA CAT CAC r Ala Gly His His 1360	CAC CAC AAC AAC CCC His His Asn Asn Pro 1365	GGC 4313 Gly
GGC GGG TAC ATG CTC AG Gly Gly Tyr Met Leu Se 1370	C AAG TCG CTC TAC r Lys Ser Leu Tyr 1375	CCT GAC CGG GTC ACG Pro Asp Arg Val Thr 1380	CAA 4361 Gln
AAC CCT TTC ATC CCC AC Asn Pro Phe Ile Pro Th 1385	T TTT GGG GAC GAC r Phe Gly Asp Asp 90	CAG TGC TTG CTC CAT Gln Cys Leu Leu His 1395	GGC 4409 Gly 1400
AGC AAA TCC TAC TTC TT Ser Lys Ser Tyr Phe Ph 1405	e Arg Gln Pro Thi	G GTG GCG GGG GCG TCG Val Ala Gly Ala Ser 0 1415	Lys
GCC AGG CCG GAC TTC CG Ala Arg Pro Asp Phe Ar 1420	G GCC CTT GTC ACG g Ala Leu Val Thi 1425	C AAC AAG CCG GTG GTC Asn Lys Pro Val Val 1430	TCG 4505 Ser
GCC CTT CAT GGG GCC GT Ala Leu His Gly Ala Va 1435	G CCA GCC CGT TTG l Pro Ala Arg Pho 1440	C CAG AAG GAC ATC TGT G Gln Lys Asp Ile Cys 1445	ATA 4553 Ile
GGG AAC CAG TCC AAC CC Gly Asn Gln Ser Asn Pr 1450	C TGT GTG CCT AAG O Cys Val Pro Ass 1455	C AAC ACA AAC CCC AGG n Asn Thr Asn Pro Arg 1460	GCT 4601 Ala
TTC AAT GGC TCC AGC AA Phe Asn Gly Ser Ser As 1465	T GGG CAT GTT TAY n Gly His Val Ty: 70	GAG AAA CTT TCT AGT Glu Lys Leu Ser Ser 1475	ATT 4649 Ile 1480
GAG TCT GAT GTC TGAGTG Glu Ser Asp Val 148	AGGG AACAGAGAGG	TTAAGGTGGG TACGGGAGGG	4701

TAAGGCTGTG	GGTCGCGTGA	TGCGCATGTC	ACGGAGGGTG	ACGGGGGTGA	ACTTGGTTCC	4761
CATTTGCTCC	TTTCTTGTTT	TAATTTATTT	ATGGGATCCT	GGAGTTCTGG	TTCCTACTGG	4821
GGGCAACCCT	GGTGACCAGC	ACCATCTCTC	CTCCTTTTCA	CAGTTCTCTC	CTTCTTCCCC	4881
CCGCTGTCAG	CCATTCCTGT	TCCCATGAGA	TGATGCCATG	GGCCCTCTCA	GCAGGGGAGG	4941
GTAGAGCGGA	GAAAGGAAGG	GCTGCATGCG	GGCTTCCTCC	TGGTGTGGAA	GAGCTCCTTG	5001
ATATCCTCTT	TGAGTGAAGC	TGGGAGAACC	AAAAAGAGGC	TATGTGAGCA	CAAAGGTAGC	5061
TTTTCCCAAA	CTGATCTTTT	CATTTAGGTG	AGGAAGCAAA	AGCATCTATG	TGAGACCATT	5121
TAGCACACTG	CTTGTGAAAG	GAAAGAGGCT	CTGGCTAAAT	TCATGCTGCT	TAGATGACAT	5181
CTGTCTAGGA	ATCATGTGCC	AAGCAGAGGT	TGGGAGGCCA	TTTGTGTTTA	TATATAAGCC	5241
CAAAAATGCT	TGCTTCAACC	CCATGAGACT	CGATAGTGGT	GGTGAACAGA	ACCCAAGGTC	5301
ATTGGTGGCA	GAGTGGATTC	TTGAACAAAC	TGGAAAGTAC	GTTATGATAG	TGTCCCCCGG	5361
TGCCTTGGGG	ACAAGAGCAG	GTGGATTGTG	CGTGCATGTG	TGTTCATGCA	CACTTGCACC	5421
CATGTGTAGT	CAGGTGCCTC	AAGAGAAGGC	AACCTTGACT	CTTTCGTTGA	ATTTGCATCT	5481
CTTCAAGACA	CAAGATTAAA	ACAAAATTTA	CGCTAAATTG	GATTTTAAAT	TATCTTC	5538

# (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1484 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu

Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro 20 25 30

Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val

Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val

Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser 65

Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly

Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu

Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly 120 115

Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe 140

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile 155 150 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly 280 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser 310 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn 425 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val 635 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys 755 760 765 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp 810 Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His

- Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile 850 855 860
- Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg 865 870 875 880
- Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser 885 890 895
- Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser 900 905 910
- Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu 915 920 925
- Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser 930 935 940
- Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser 945 950 955 960
- Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys 965 970 975
- Asp Ser Asn Val Tyr Gln Asp His Tyr His His His Arg Pro His 980 985 990
- Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn 995 1000 1005
- Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp 1010 1015 1020
- Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly 1025 1030 1035 1040
- Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile 1045 1050 1055
- Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn 1060 1065 1070
- Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser 1075 1080 1085
- Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu 1090 1095 1100
- Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys 1105 1110 1115 1120
- Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln 1125 1130 1135
- Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr 1140 1145 1150
- Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser 1155 1160 1165
- Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly 1170 1175 1180
- Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn 1185 1190 1195 1200

- Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg 1210 1205
- Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln 1225
- Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala
- Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp 1255
- Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys 1280 1275 1270
- Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn 1290 1285
- Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys 1305
- Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly 1320
- Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala 1335
- Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly 1350 1355 1345
- His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser 1365
- Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly 1385 1380
- Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln 1400
- Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
- Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
- Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val 1450
- Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His 1465
- Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val 1480 1475
- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4695 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: both (D) TOPOLOGY: both
  - (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCGA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCCCC CGGGGCCTGC CCCCGACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCCTGGCC	420
CCCCCCCAT CCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG  Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys  1 5 10 15	529
ATG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG Met Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu 20 25 30	577
GCG CCG GGG CCG GGC GGC GGC GGC GGC GGC	625
GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala 50 55 60	673
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser 65 70 75	721
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp 80 85 90 95	769
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg 100 105 110	817
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCC GCC GCC GCC GCC Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala 115 120 125	865
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser 130 135 140	913
GAG CAC GGC GGC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser 145 150 155	961
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile 160 165 170 175	1009

					GAG Glu												1057
					CAC His												1105
ACT Thr	GAC Asp	GGC Gly 210	AGT Ser	CTG Leu	GTG Val	GGC Gly	TGG Trp 215	GAG Glu	CAC His	CGC Arg	GGA Gly	GCG Ala 220	CTG Leu	ACG Thr	CTG Leu		1153
					GAG Glu												1201
					CTG Leu 245												1249
					GAG Glu												1297
					CCC Pro												1345
					CTT Leu												1393
					TCG Ser												1441
					GCC Ala 325												1489
					CTT Leu												1537
					GGG Gly												1585
ACG Thr	TGG Trp	GAT Asp 370	AAC Asn	CGG Arg	GAT Asp	TAC Tyr	TCC Ser 375	TTC Phe	AAT Asn	GAG Glu	GAC Asp	GGC Gly 380	TTC Phe	CTA Leu	GTG Val		1633
AAC Asn	CCC Pro 385	TCC Ser	CTG Leu	GTG Val	GTC Val	ATC Ile 390	TCC Ser	CTC Leu	ACC Thr	AGA Arg	GAC Asp 395	AGG Arg	ACG Thr	TGG Trp	GAG Glu		1681
GTG Val 400	GTG Val	GGC Gly	AGC Ser	TGG Trp	GAG Glu 405	CAG Gln	CAG Gln	ACG Thr	CTC Leu	CGC Arg 410	CTC Leu	AAG Lys	TAC Tyr	CCG Pro	CTG Leu 415		1729
					CGC Arg												1777
					CTG Leu											:	1825

					GGC Gly											1873
AGC Ser	CAG Gln 465	CTC Leu	AAC Asn	CGA Arg	ACC Thr	CAC His 470	AGC Ser	CCT Pro	CCA Pro	CCG Pro	GAT Asp 475	GCC Ala	CCC Pro	CGC Arg	CCG Pro	1921
GAA Glu 480	AAG Lys	CGC Arg	TGC Cys	TGC Cys	AAG Lys 485	GGT Gly	TTC Phe	TGC Cys	ATC Ile	GAC Asp 490	ATT Ile	CTG Leu	AAG Lys	CGG Arg	CTG Leu 495	1969
					TTC Phe											2017
AAG Lys	CAC His	GGA Gly	AAG Lys 515	AAG Lys	ATC Ile	GAT Asp	GGC Gly	GTC Val 520	TGG Trp	AAC Asn	GGC Gly	ATG Met	ATC Ile 525	GGG Gly	GAG Glu	2065
GTG Val	TTC Phe	TAC Tyr 530	CAG Gln	CG <u>Ç</u> Arg	GCA Ala	GAC Asp	ATG Met 535	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu 540	ACC Thr	ATC Ile	AAC Asn	2113
GAG Glu	GAG Glu 545	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTG Val 550	GAC Asp	TTC Phe	TCC Ser	GTC Val	CCC Pro 555	TTC Phe	GTG Val	GAG Glu	ACC Thr	2161
					GTG Val 565											2209
GCC Ala	TTC Phe	CTC Leu	GAG Glu	CCC Pro 580	TAC Tyr	AGC Ser	CCC Pro	GCC Ala	GTG Val 585	TGG Trp	GTG Val	ATG Met	ATG Met	TTC Phe 590	GTC Val	2257
					GTC Val											2305
					AAC Asn											2353
					ATT Ile					Trp						2401
					GTG Val 645											2449
					GTG Val											2497
					CTG Leu											2545
					CTC Leu											2593
					AAG Lys											2641

	AAC Asn															2689
	AAC Asn															2737
	CTG Leu															2785
	AAG Lys															2833
	GCC Ala 785															2881
AAG Lys 800	CGG Arg	CCC Pro	ATC Ile	GAC.	CTG Leu 805	GCG Ala	TTG Leu	CTG Leu	CAG Gln	TTC Phe 810	CTG Leu	GGG Gly	GAT Asp	GAT Asp	GAG Glu 815	2929
	GAG Glu															2977
	ATC Ile															3025
	TTC Phe															3073
	TGG Trp 865															3121
	CAC His															3169
	TGC Cys															3217
	CAG Gln															3265
	CCC Pro															3313
	CGG Arg 945															3361
	TTC Phe															3409
	CTG Leu															3457

CT(	TCC Ser	CCG Pro	CCG Pro 995	GCC Ala	GCT	CAG Gln	CCC	CCG Pro	Gln	AAG Lys	CCC Pro	CCG Pro	GCC Ala 100	Ser	TAT	3505
TTC Phe	GCC Ala	ATC Ile 101	GTA Val O	CGC Arg	GAC Asp	AAG Lys	GAG Glu 101	Pro	GCC Ala	GAG Glu	CCC Pro	CCC Pro	Ala	GGC	GCC Ala	3553
TTC Phe	CCC Pro 102	Gly	TTC Phe	CCG	TCC Ser	CCG Pro 103	Pro	GCG Ala	CCC	ccc Pro	GCC Ala 103	Ala	GCG Ala	GCC Ala	ACC Thr	3601
GCC Ala 104	Val	GGG Gly	CCG Pro	CCA Pro	CTC Leu 104	Cys	CGC Arg	TTG Leu	GCC Ala	TTC Phe 105	Glu	GAC Asp	GAG Glu	AGC Ser	CCG Pro 1055	3649
CCG Pro	GCG Ala	CCC Pro	GCG Ala	CGG Arg 106	Trp	CCG Pro	CGC Arg	TCG Ser	GAC Asp 106	Pro	GAG Glu	AGC Ser	CAA Gln	CCC Pro 107	Leu	3697
CTG Leu	GGG Gly	CCA Pro	GGC Gly 1075	Ala	GGC Gly	GGC Gly	GCG Ala	GGG Gly 108	Gly	ACG Thr	GGG Gly	GGC Gly	GCA Ala 108	Gly	GGA Gly	3745
GGA Gly	GCC Ala	Pro	GCC Ala O	GCT Ala	ccg Pro	ccc Pro	CCG Pro 109	Cys	TTC Phe	GCC Ala	GCG Ala	CCG Pro 110	Pro	CCG Pro	TGC Cys	3793
TTT Phe	TAC Tyr 110	Leu	GAT Asp	GTC Val	GAC Asp	CAG Gln 1110	Ser	CCG Pro	TCG Ser	GAC Asp	TCG Ser 111	Glu	GAC Asp	TCG Ser	GAG Glu	3841
AGC Ser 112	Leu	GCC Ala	GGC Gly	GCG Ala	TCC Ser 112	Leu	GCC Ala	GGC Gly	CTG Leu	GAT Asp 113	Pro	TGG Trp	TGG Trp	TTC Phe	GCC Ala 1135	3889
GAC Asp	TTC Phe	CCT Pro	TAC Tyr	CCG Pro 1140	Tyr	GCC Ala	GAT Asp	CGC Arg	CTC Leu 114	Gly	CSG Xaa	CCC Pro	GCG Ala	GCA Ala 1150	Arg	3937
TAC Tyr	GGA Gly	TTG Leu	GTC Val 1155	Asp	AAA Lys	CTA Leu	GGG Gly	GGC Gly 1160	Trp	CTC Leu	GCC Ala	GGG Gly	AGC Ser 1165	Trp	GAC Asp	3985
TAC Tyr	Leu	CCT Pro 1170	CCS Xaa )	CGC Arg	Ser	GGT Gly	Arg	Ala	GCC Ala	TGG Trp	CAC His	TGT Cys 1180	Arg	CAC His	TGC Cys	4033
GCC Ala	AGC Ser 118	Leu	GAG Glu	CTG Leu	CTT Leu	CCG Pro 1190	Pro	CCG Pro	CGC Arg	CAT His	CTC Leu 1195	Ser	TGC Cys	TCG Ser	CAC His	4081
GAT Asp 1200	Gly	CTG Leu	GAC Asp	GGC Gly	GGC Gly 1205	Trp	TGG Trp	GCG Ala	CCA Pro	CCG Pro 1210	Pro	CCA Pro	CCC Pro	TGG Trp	GCC Ala 1215	4129
GCC Ala	GGG Gly	CCC Pro	CTG Leu	ccc Pro 1220	Arg	CGC Arg	CGG Arg	GCC Ala	CGC Arg 1225	Cys	GGG Gly	TGC Cys	CCG Pro	CGG Arg 1230	Ser	4177
CAC His	CCG Pro	CAC His	CGC Arg : 1235	CCG Pro	CGG Arg	GCC Ala	Ser	CAC His 1240	Arg	ACG Thr	CCC Pro	GCC Ala	GCT Ala 1245	Ala	GCG Ala	4225
CCC Pro	CAC His	CAC His 1250	CAC /	AGG Arg	CAC His	Arg	CGC Arg 1255	GCC Ala	GCT Ala	GGG Gly	GGC Gly	TGG Trp 1260	Asp	CTC Leu	CCG Pro	4273

		GCG Ala					Ser					Ser				43	321
CGC Arg 1280	Ala	GCC Ala	CCT Pro	GCG Ala	CGC Arg 1285	Arg	CTT Leu	ACC Thr	GGG Gly	CCC Pro 1290	Ser	CGC Arg	CAC His	GCT Ala	CGC Arg 1295	43	369
		CCG Pro			Ala					Pro					Ser	44	417
CAC His	CGG Arg	AGA Arg	CAC His 131	Arg	GGC	GGG Gly	GAC Asp	CTG Leu 1320	Gly	ACC Thr	CGC Arg	AGG Arg	GGC Gly 132	Ser	GCG Ala	44	465
		TCT Ser 1330	Ser					Val	TGAC	CGCGC	GCC (	CCGG	GGC	cc		45	512
CAC	CGCC	ccc 1	TGG	CĀĢ	CG CA	AGGC	CACGO	G CC	CGAGO	GGG	CGC	CCGC	AGT (	GAC	AGGĀCC	4!	572
CGC	STGG	TT C	GGA	AGGA	AA GO	CAGTO	GAAG	C TG	cccc	GACC	CCG	CCTG	GAG (	CAGC	STCCTG	4	632
CGC	ccci	rgg 1	TCTC	GAGG	SA AC	CCGC	AAGC	G GGZ	AGAGO	FATT	TGG	rccc	CA A	ACTA	CACCC	40	692
AGG																4	695

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1336 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met
1 10 15

Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala 20 25 30

Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala 35 40 45

Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala 50 55 60

Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser Pro 65 70 75 80

Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro 85 90 95

Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val 100 105 110

His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro 115 120 125

Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu 130 135 140 His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe 170 165 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala Pro 280 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu 295 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn 340 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val 390 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu 470 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val 520 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly 555 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met 585 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser 600 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln 695 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys 825 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val

Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala 850 855 860

Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr 865 870 875 886

His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys 885 890 895

Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro 900 905 910

Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly 915 920 925

Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg 930 935 940

Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly 945 950 955 960

Phe His Arg Tyr Tyr-Gly Pro Ile Glu Pro Gln Gly Leu Gly 965 970 975

Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu 980 985 990

Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe 995 1000 1005

Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe 1010 1020

Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala 1025 1030 1035 1040

Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro 1045 1050 1055

Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu 1060 1065 1070

Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly 1075 1080 1085

Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe 1090 1095 1100

Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser 1105 1110 1115 1120

Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Phe Ala Asp 1125 1130 1135

Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr 1140 1145 1150

Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr 1155 1160 1165

Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala 1170 1175 1180

Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp 1185 1190 1195 1200

Gly	Leu	Asp	Gly	Gly 120		Trp	Ala	Pro	Pro 1210		Pro	Pro	Trp	Ala 1219		
Gly	Pro	Leu	Pro 1220	Arg )	Arg	Arg	Ala	Arg 1225		Gly	Сув	Pro	Arg 1230		His	
Pro	His	Arg 1235		Arg	Ala	Ser	His 1240		Thr	Pro	Ala	Ala 1245		Ala	Pro	
His	His 1250	His )	Arg	His	Arg	Arg 1255		Ala	Gly	Gly	Trp 1260		Leu	Pro	Pro	
Pro 1265	Ala	Pro	Thr	Ser	Arg 1270		Leu	Glu	Asp	Leu 1275		Ser	Сув	Pro	Arg 1280	
Ala	Ala	Pro	Ala	Arg 1285		Leu	Thr	Gly	Pro 1290		Arg	His	Ala	Arg 1295	_	
Суз	Pro	His	Ala 1300		His	Trp	Gly	Pro 1305		Leu	Pro	Thr	Ala 1310		His	
Arg	Arg	His 1315		Gľý	Gly	Asp	Leu 1320		Thr	Arg	Arg	Gly 1325		Ala	HĪs	
Phe	Ser 1330		Leu	Glu	Ser	Glu 1335										
(2) INFORMATION FOR SEQ ID NO:17:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 71 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA																
	(xi)	SEQ	UENC	E DE	scri	PTIO	N: S	EQ I	D NO	:17:						
GGGI	GGCG	GC C	GCAG	AGCA	C CT	CCAC	CATC	TCC	TTGT	CCT	ACTO	CAAG	AT C	TGGC	CCTAG	60
TCCA	TGTT	TG C														71
(2)	INFO	RMAT	ION	FOR	SEQ	ID N	0:18	:								
	(i)	(A (B (C	) LE ) TY ) ST	E CH NGTH PE: RAND POLO	: 71 nucl EDNE	bas eic SS:	e pa acid both	irs								
	(ii)	MOL	ECUL	E TY	PE:	cDNA										
	(xi)	SEQ	UENC	E DE	SCRI	PTIO:	N: S	EQ I	D NO	:18:						
TGGT	GGTC	cc c	AACC'	TGTA	G GA	CTTG	GTTC	TGG	AGGA	GGA '	TCTG	GTGT	AG G	CAAA	CATGG	60
ACTA	GGGC	CA G														71

(2) INFORMATION FOR SEQ ID NO:19:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 61 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG	60
G	61
(2) INFORMATION FOR SEQ ID NO:20:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 62 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
CGTGAGACGT CAGACAAAGG AGGCCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT	60
CT	62
(2) INFORMATION FOR SEQ ID NO:21:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 195 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
CCGCAGAGCA CCTCCACCAT CTCCTTGTCC TACTCCAAGA TCTGGCCCTA GTCCATGTTT	60
GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG	120
TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC	180
TCCTTTGTCT GACGT	195